

Genbank version 4.5
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Membrane protein search using SW model

Membrane protein search using SW model
September 4, 2002 19:50:14 : Search time 13:13.9 seconds
(without alignments)
160,950 Million coil updates/sec

Filter:
Percent scores 14
Sequences 11119mmmmmmmmmm 14

Scoring table:
gapop 10.0 / gapext 1.0

Search:
1797656 seqs, 1045329254 residues

Total number of hits satisfying chosen parameters: 294512

Minimum hit seq length: 0
Maximum hit seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database:
1: gp_ha:*
2: gp_hf:*
3: gp_hg:*
4: gp_hm:*
5: gp_hn:*
6: gp_ho:*
7: gp_hp:*
8: gp_hq:*
9: gp_hr:*
10: gp_hs:*
11: gp_hs:*
12: gp_hs:*
13: gp_hs:*
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27: gp_hs:*
28: gp_hs:*
29: gp_hs:*
30: gp_hs:*
31: gp_hs:*
32: gp_hs:*
33: gp_hs:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Match Length DB Hit Description

Result	Query	Match	Length	DB	Hit	Description
1	AK03568	42.3	15	6	AK03568	AK03568 Sequence
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3	AK03568	42.3	15	6	AK03568	AK03568 Sequence
4	AK03568	42.3	15	6	AK03568	AK03568 Sequence
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8	AK03568	42.3	15	6	AK03568	AK03568 Sequence
9	AK03568	42.3	15	6	AK03568	AK03568 Sequence
10	AK03568	42.3	15	6	AK03568	AK03568 Sequence
11	AK03568	42.3	15	6	AK03568	AK03568 Sequence
12	AK03568	42.3	15	6	AK03568	AK03568 Sequence
13	AK03568	42.3	15	6	AK03568	AK03568 Sequence
14	AK03568	42.3	15	6	AK03568	AK03568 Sequence
15	AK03568	42.3	15	6	AK03568	AK03568 Sequence
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18	AK03568	42.3	15	6	AK03568	AK03568 Sequence
19	AK03568	42.3	15	6	AK03568	AK03568 Sequence
20	AK03568	42.3	15	6	AK03568	AK03568 Sequence
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ALIGNMENTS

Result 1
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Sequence 344 from Patent US 5869254
AK03568
AK03568.1 GI:5949174
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 15)
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE
BASE COUNT
6 a 4 c 3 d 2 t
ORIGIN

Query Match 12.98 Score 62 DB 42 Length 15
Best Local Similarity 42.98 Prod. No. 10062

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1b	1-111	111-144	144-177	177-210	210-243	
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ABSTRACT 1	1-111	111-144	144-177	177-210	210-243	
DEFINITION	1-111	111-144	144-177	177-210	210-243	
ABSTRACT 2	1-111	111-144	144-177	177-210	210-243	
DEFINITION	1-111	111-144	144-177	177-210	210-243	
ABSTRACT 3	1-111	111-144	144-177	177-210	210-243	
DEFINITION	1-111	111-144	144-177	177-210	210-243	
ABSTRACT 4	1-111	111-144	144-177	177-210	210-243	
DEFINITION	1-111	111-144	144-177	177-210	210-243	
ABSTRACT 5	1-111	111-144	144-177	177-210	210-243	
DEFINITION	1-111	111-144	144-177	177-210	210-243	
ABSTRACT 6	1-111	111-144	144-177	177-210	210-243	
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DEFINITION	1-111	111-144	144-177	177-210	210-243	
ABSTRACT 81	1-111	111-144	144-177	177-210	210-243	
DEFINITION	1-111	111-144	144			

[illegible]


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db 14 TTGGATATTCAG 1
RESULT 10
LOCUS 151797
DEFINITION Sequences 44 from Patient US 561054.
ACCESSION 151797.1 GI:2182061
KEYWORDS
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ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT 6 a 4 c 4 g 2 t
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Best Local Similarity 42.9%; Pred. No. 10:06;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;
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db 15 TTGGATATTCAG 2
RESULT 11
LOCUS AX132920
DEFINITION Sequence 4188 from Patient W0130362.
ACCESSION AX132920
VERSION AX132920.1 GI:1419240
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT 0 a 4 c 4 g 6 t
ORIGIN
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Best Local Similarity 42.9%; Pred. No. 10:06;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;
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db 15 TTGGATATTCAG 2
RESULT 12
LOCUS AX041470
DEFINITION Synthetic oligonucleotide primer. HaeIII/HaeIII.
ACCESSION AX041470
VERSION AX041470.1 GI:1749600
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS
TITLE
JOURNAL

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ACCESSION A05414
VERSION A05414.1 GI:512617
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT 8 a 2 c 4 g 4 t
ORIGIN
Query Match 42.9% Score 6; DB 6; Length 17;
Best Local Similarity 42.9%; Pred. No. 10:06;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;
db 14 TTGGATATTCAG 1
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db 14 TTGGATATTCAG 1
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LOCUS A09621
DEFINITION Oligonucleotide.
ACCESSION A09621
VERSION A09621.1 GI:490594
KEYWORDS
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ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS
TITLE
JOURNAL
FEATURES
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Best Local Similarity 42.9%; Pred. No. 10:06;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;
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RESULT 14
LOCUS AR046419
DEFINITION Sequence 1212 from Patient US 5817796.
ACCESSION AR046419
VERSION AR046419.1 GI:5967884
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS
TITLE
JOURNAL

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2

3

4

11 Mutative Adairie J., Jarvis L., Thompson JB., Wincott P.
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 13 WP1: 1996-09643/43.
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RESULT 12
AA47804/
ID AAF47804 standard; DNA: 15 BP.
XX
AC AAF47804:
XX
DE 30-MAR-2001 (first entry)
XX
DE IGFBP2 oligonucleotide #1140.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriasis;
KW cytostatic; dermatologically; cardially; vitreoid; ophthalmologically; keloid;
KW skin disorder; insulin-like growth factor 1 receptor; IGF-1; psoriasis;
KW skin binding protein; IGFBP-2; IGFBP; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; scleroderma; rubea;
KW keratosis; neoplasia; scleroderma; warts; skin cancer; sclerotic disease;
KW hyperneovascular condition of the retina; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN W0200078341-A1.
XX
PD 28-DEC-2000.
XX
PI 21-JUN-2000; 2000WD-A000693.
XX
PR 21-JUN-1999; 9908-0140445.
XX
PA (MORF) MORFACH CHILDRENS RES INST.
XX
PI Wright CJ, Werther GA, Edmondson SK;
XX
DE WP1: 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by
PT administering UV (ultra-violet) treatment (optional) and an antisense
PT nucleic acid that inhibits or reduces growth factor mediated cell
PT proliferation and/or inflammation -
XX
PS Example 6; Page 41; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects
CC of skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for insulin-like growth factor [IGF] 1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF47804 and
CC AAF47805/6). The method is useful for ameliorating the effects of
CC psoriasis, ichthyosis, pityriasis, rubea, pilaris, scleroderma, keloids,
CC keratosis, neoplasia, scleroderma, warts, benign growths, cancers of the
CC skin, a hyperneovascular condition such as a neovascular condition of the
CC retina, brain or skin, growth factor mediated malignancies, other
CC sclerotic disease, kidney disease, hyperproliferation of the inside of
CC blood vessels or any other hyperplasia.
XX
XX Sequence 15 BP; 3 A; 9 C; 1 G; 2 T; 0 other;

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Query Match 42.98; Score 6; BR 22; Length 15;
Best Local Similarity 42.98; Pred. No. 8,1e+04;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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07 1 ttgmmmmmmmm 14
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DB 14 ttgagagagggc 1

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RESULT 13
AA47804/6
ID AAF47804 standard; DNA: 15 BP.

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XX
AC AAF47804:
XX
DE 30-MAR-2001 (first entry)
XX
DE IGFBP3 oligonucleotide #1224.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriasis;
KW cytostatic; dermatologically; cardially; vitreoid; ophthalmologically; keloid;
KW skin disorder; insulin-like growth factor 1 receptor; IGF-1; psoriasis;
KW skin binding protein; IGFBP-2; IGFBP; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; scleroderma; rubea;
KW keratosis; neoplasia; scleroderma; warts; skin cancer; sclerotic disease;
KW hyperneovascular condition of the retina; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN W0200078341-A1.
XX
PD 28-DEC-2000.
XX
PI 21-JUN-2000; 2000WD-A000693.
XX
PR 21-JUN-1999; 9908-0140445.
XX
PA (MORF) MORFACH CHILDRENS RES INST.
XX
PI Wright CJ, Werther GA, Edmondson SK;
XX
DE WP1: 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by
PT administering UV (ultra-violet) treatment (optional) and an antisense
PT nucleic acid that inhibits or reduces growth factor mediated cell
PT proliferation and/or inflammation -
XX
PS Example 7; Page 52; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects
CC of skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for insulin-like growth factor [IGF] 1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF47804 and
CC AAF47805/6). The method is useful for ameliorating the effects of
CC psoriasis, ichthyosis, pityriasis, rubea, pilaris, scleroderma, keloids,
CC keratosis, neoplasia, scleroderma, warts, benign growths, cancers of the
CC skin, a hyperneovascular condition such as a neovascular condition of the
CC retina, brain or skin, growth factor mediated malignancies, other
CC sclerotic disease, kidney disease, hyperproliferation of the inside of
CC blood vessels or any other hyperplasia.
XX
XX Sequence 15 BP; 4 A; 5 C; 1 G; 5 T; 0 other;

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Query Match 42.98; Score 6; BR 22; Length 15;
Best Local Similarity 42.98; Pred. No. 8,1e+04;
Matches 6; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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07 1 ttgmmmmmmmm 14
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DB 15 ttgagagagggc 2

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RESULT 14
AA47805/6
ID AAF47805 standard; DNA: 15 BP.
XX
AC AAF47805:
XX

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GenCore version 4.5
Copyright (c) 1993 2000 Campanen Ltd.

0M nucleic nucleic search, using SW model

Run on: September 22, 2002, 22:51:17 : Search time 42.9 seconds
(without alignments)
80.160 Million cell updates/sec

Title: US-09-530-935 1

Sequence: 1 Ulyssiananinca 14

Scoring table: IDENTITY_NOC

Gapop 10.0 / Gapext 1.0

Searched: 38353 seqs, 12816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: Issued_Patents_NA:
1: US-08-182-968A-334 seq.
2: US-08-182-968A-334 seq.
3: US-08-182-968A-334 seq.
4: US-08-182-968A-334 seq.
5: US-08-182-968A-334 seq.
6: US-08-182-968A-334 seq.
7: US-08-182-968A-334 seq.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	42.9	15	US-08-182-968A-334	Sequence 334, App
2	6	42.9	15	US-08-182-968A-334	Sequence 334, App
3	6	42.9	15	US-08-182-968A-334	Sequence 334, App
4	6	42.9	15	US-08-182-968A-334	Sequence 334, App
5	6	42.9	15	US-08-182-968A-334	Sequence 334, App
6	6	42.9	15	US-08-182-968A-334	Sequence 334, App
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44	6	42.9	15	US-08-182-968A-334	Sequence 334, App
45	6	42.9	15	US-08-182-968A-334	Sequence 334, App

ALIGNMENTS

RESULT 1
US-08-182-968A-334/c
Sequence 334, Application US/08182968A
Patent No. 5610054
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: IDENTIFYING HEMATITIS G
TYPE OF INVENTION: VITRO PATENT
NUMBER OF SEQUENCES: 497
SEQUENCE IDENTIFICATION ADDRESS:
ADDRESS: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Walburg, Richard J.
FILING DATE: 13 JANUARY 1994
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NO.: 08/092,888
FILING DATE: 14 MAY 1992
ATTORNEY/AGENT INFORMATION:
NAME: Walburg, Richard J.
FILING DATE: 13 JANUARY 1994
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NO.: 08/092,888
FILING DATE: 14 MAY 1992
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
FAX: 67 3510
INFORMATION FOR SEQ ID NO. 434:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STANDARDS: single
TOPOLOGY: linear
US-08-182-968A-334

Query Match: 42.9% Score: 60 DB ID: Length: 15
Best Local Similarity: 42.9% Pred. No.: 10004
Seq ID: 15 Seq Length: 15 Mismatch: 0 Indels: 0

Query Match 42.9%; Score 6; MB 4; Length 15

Sequence 13b, Appendix
Patent No. 6194150
GENERAL INFORMATION

APPLICANT: STEUBOONT, Daniel F.
APPLICANT: Mowbray, Thale
TITLE OF EVENT: MEETING AND TRAINING FOR THE
TITLE OF EVENT IN INDIGENOUS CULTURAL HERITAGE
TITLE OF EVENT IS AN REVEALAL OF INDIGENOUS KNOW-
LEDGE OF SCIENTISTS. 2751
PREFERENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Santa Fe 87001
STATE: Los Angeles
STATE: California
COUNTRY: U.S.A.
PHONE: 960071
OFFICE REMARKS: F.B.I.
METHOD TYPE: 4.5% HPLC 100 1.14 ml
MEDIUM TYPE: 200 g/l
COMMENTS: 100 mg/ml H₂O
OPERATING SYSTEM: IBM PC 2.0 5.0
SOFTWARE: FAST SEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 02-000000-003
FILING DATE:
FOR APPLICATION DATA:
APPLICATION NUMBER: 08/085,684
FILING DATE:
ALTERED/ACTING INFORMATION:
NAME: Mowbray, Richard
REGISTRATION NUMBER: 42,427
REFERENCE: 4111 II PAGE: 2,9,278
TELECOMMUNICATION INFORMATION:
TELEPHONE: (214) 489-1600
TELEX: (214) 965-0443
FAX: 67 6510
INFORMATION FOR SEQ ID NO.: 146;
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
COMPOSITION: 11004T
GC CONTENT: 43.33%

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Search completed: September 4, 2002, 2:45:29
Job Number: 6442800
